

IN THE SPECIFICATION:

Please incorporate the enclosed paper copy of the substitute SEQUENCE LISTING into the application on the page following the Abstract.

Furthermore, please amend paragraph number [0020] as follows:

[0020] In such an embodiment, the peptide can have a formula selected from the group consisting of VLPALP (SEQ ID NO:3), the derivative ALPALP (SEQ ID NO:21), the derivative VAPALP (SEQ ID NO:22), the derivative ALPALPQ (SEQ ID NO:23), the derivative VLPAAPQ (SEQ ID NO:24), the derivative VLPALAQ (SEQ ID NO:25), the derivative VLPALA (SEQ ID NO:28), VLPALPQ (SEQ ID NO:29), the derivative VLPALPA (SEQ ID NO:31), the derivative GVLPALP (SEQ ID NO:32), and the derivative VLAALP (SEQ ID NO:47 27).

Please amend paragraph number [0058] as follows:

[0058] A non-extensive list of relevant oligopeptides useful for application in a method and/or database according to the invention include:

Accession number pdb|1DE7|1DE7-A, *see* INTERACTION OF FACTOR XIII ACTIVATION PEPTIDE WITH ALPHA- THROMBIN, *J Biol. Chem.* 2000 275(47):36942-8, which includes LQGV (SEQ ID NO:1), LQGVV (SEQ ID NO:53), and LQGVVP (SEQ ID NO:54);

Accession number pdb|1DL6|1DL6-A (*see also* Accession number Q00403) SOLUTION STRUCTURE OF HUMAN TFIIIB N-TERMINAL DOMAIN, including LDALP (SEQ ID NO:55);

Accession number pdb|1QMH|1QMH-A, *see* CRYSTAL STRUCTURE OF RNA 3'-TERMINAL PHOSPHATE CYCLASE, AN UBIQUITOUS ENZYME (accession number NP_709195), which includes LQTV (SEQ ID NO:56), VLPAL (SEQ ID NO:8), and LVLQTVLPAL (SEQ ID NO:57);

Accession number pdb|1LYP|1LYP, CAP18 (RESIDUES 106 - 137), which includes IQG, IQGL (SEQ ID NO:58), LPKL (SEQ ID NO:59), and LLPKL (SEQ ID NO:60);

Accession number pdb|1B9O|1B9O-A HUMAN ALPHA-LACTALBUMIN (accession

number P00709), which includes LPEL (SEQ ID NO:61);

Accession number pdb|1GLU|1GLU-A GLUCOCORTICOID RECEPTOR (DNA-BINDING DOMAIN) (accession number P06536), which includes PARP (SEQ ID NO:62);

Accession number pdb|2KIN|2KIN-B KINESIN (MONOMERIC) FROM RATTUS NORVEGICUS (*see also*, accession number P56536), which includes MTRI (SEQ ID NO:63);

Accession number pdb|1SMP|1SMP-I MOL_ID: 1; MOLECULE: SERRATIA METALLO PROTEINASE; CHAIN: A (*see also*, accession number P18958), which includes LQKL (SEQ ID NO:64), LQKLL (SEQ ID NO:65), PEAP (SEQ ID NO:66), and LQKLLPEAP (SEQ ID NO:67);

Accession number pdb|1ES7|1ES7-B COMPLEX BETWEEN BMP-2 AND TWO BMP RECEPTOR IA ECTODOMAINS (*see also*, accession numbers P36894 and P12643), which includes LPQ, PTLP (SEQ ID NO:68), and LQPTL (SEQ ID NO:69);

Accession number pdb|1BHX|1BHX-F X-RAY STRUCTURE OF THE COMPLEX OF HUMAN ALPHA THROMBIN WITH THE INHIBITOR SDZ 229-357 (*see also*, accession number P00734), which includes LQV, and LQVV (SEQ ID NO:70);

Accession number pdb|1VCB|1VCB-A THE VHL-ELONGINC-ELONGINB STRUCTURE (*see also*, accession number BI067547 for the nucleotide sequence), which includes PELP (SEQ ID NO:71);

Accession number pdb|1CQK|1CQK-A CRYSTAL STRUCTURE OF THE CH3 DOMAIN FROM THE MAK33 ANTIBODY (*see also*, accession number 1CQKB), which includes PAAP (SEQ ID NO:72), PAAPQ (SEQ ID NO:73), and PAAPQV (SEQ ID NO:74);

Accession number pdb|1FCB|1FCB-A FLAVOCYTOCHROME (*see also*, accession number P00175), which includes LQG;

Accession number pdb|1LDC|1LDC-A L-LACTATE DEHYDROGENASE: CYTOCHROME C OXIDOREDUCTASE (FLAVOCYTOCHROME B=2=) (E.C.1.1.2.3) MUTANT WITH TYR 143 REPLACED BY PHE (Y143F) COMPLEXED WITH PYRUVATE (*see also*, accession number P00175), which includes LQG;

Accession number pdb|1BFB|1BFB BASIC FIBROBLAST GROWTH FACTOR COMPLEXED WITH HEPARIN TETRAMER FRAGMENT, which includes LPAL (SEQ ID

NO:183), PALP (SEQ ID NO:184), and PALPE (SEQ ID NO:77);

Accession number pdb|1MBF|1MBF MOUSE C-MYB DNA-BINDING DOMAIN REPEAT 1, which includes LPN;

Accession number pdb|1R2A|1R2A-A THE MOLECULAR BASIS FOR PROTEIN KINASE A (*see also*, accession number P12367), which includes LQG, and LTELL (SEQ ID NO:78);

Accession number pdb|1CKA|1CKA-B C-CRK (N-TERMINAL SH3 DOMAIN) (C-CRKSH3-N) COMPLEXED WITH C3G PEPTIDE (PRO-PRO-PRO-ALA-LEU-PRO-PRO-LYS-LYS-ARG) (*see also*, accession number Q64010), which includes PALP (SEQ ID NO:184);

Accession number pdb|1RLQ|1RLQ-R C-SRC (SH3 DOMAIN) COMPLEXED WITH THE PROLINE-RICH LIGAND RLP2 (RALPPLPRY) (NMR, MINIMIZED AVERAGE STRUCTURE) (*see also*, accession number P00523), which includes LPPL (SEQ ID NO:80), and PPLP (SEQ ID NO:81);

Accession number pdb|1TNT|1TNT MU TRANSPOSASE (DNA-BINDING DOMAIN) (NMR, 33 STRUCTURES) (*see also*, accession number GI:999952), which includes LPG, LPGL (SEQ ID NO:82), and LPK;

Accession number pdb|1GJS|1GJS-A SOLUTION STRUCTURE OF THE ALBUMIN BINDING DOMAIN OF STREPTOCOCCAL PROTEIN G (*see also*, accession number P19909), which includes LAAL (SEQ ID NO:83), and LAALP (SEQ ID NO:84);

Accession number pdb|1GBR|1GBR-B GROWTH FACTOR RECEPTOR-BOUND PROTEIN 2 (GRB2, N-TERMINAL SH3 DOMAIN) COMPLEXED WITH SOS-A PEPTIDE (NMR, 29 STRUCTURES) (*see also*, accession number Q60631), which includes LPKL (SEQ ID NO:59), and PKLP (SEQ ID NO:85);

Accession number pdb|1A78|1A78-A COMPLEX OF TOAD OVARY GALECTIN WITH THIO-DIGALACTOSE (*see also*, accession number P56217), which includes VLPSIP (SEQ ID NO:86);

Accession number pdb|1ISA|1ISA-A IRON(II) SUPEROXIDE DISMUTASE (E.C.1.15.1.1) (*see also*, accession number P09157), which includes LPAL (SEQ ID NO:183),

and PALP (SEQ ID NO:184);

Accession number pdb|1FZV|1FZV-A THE CRYSTAL STRUCTURE OF HUMAN PLACENTA GROWTH FACTOR-1 (PLGF-1), AN ANGIOGENIC PROTEIN AT 2.0A RESOLUTION (*see also*, accession number P49763), which includes PAVP (SEQ ID NO:311), and MLPAVP (SEQ ID NO:87);

Accession number pdb|1JLI|1JLI HUMAN INTERLEUKIN 3 (IL-3) MUTANT WITH TRUNCATION AT BOTH N- AND C-TERMINI AND 14 RESIDUE CHANGES, NMR, MINIMIZED AVERAGE (*see also*, accession number GI:2392392), which includes LPC, LPCL (SEQ ID NO:88), and PCLP (SEQ ID NO:89);

Accession number pdb|1HSS|1HSS-A 0.19 ALPHA-AMYLASE INHIBITOR FROM WHEAT (*see also*, accession number P01085), which includes VPALP (SEQ ID NO:90);

Accession number pdb|3CRX|3CRX-A CRE RECOMBINASE/DNA COMPLEX INTERMEDIATE I (*see also*, accession number P06956), which includes LPA, LPAL (SEQ ID NO:183), and PALP (SEQ ID NO:184);

Accession number pdb|1PRX|1PRX-A HORF6 A NOVEL HUMAN PEROXIDASE ENZYME (*see also*, accession number P30041), which includes PTIP (SEQ ID NO:91), and VLPTIP (SEQ ID NO:92);

Accession number pdb|1RCY|1RCY RUSTICYANIN (RC) FROM THIOBACILLUS FERROOXIDANS (*see also*, accession number GI:2194027), which includes VLPGFP (SEQ ID NO:93);

Accession number pdb|1A3Z|1A3Z REDUCED RUSTICYANIN AT 1.9 ANGSTROMS (*see also*, accession number GI:3402027), which includes PGFP (SEQ ID NO:94), and VLPGFP (SEQ ID NO:93);

Accession number pdb|1GER|1GER-A GLUTATHIONE REDUCTASE (E.C.1.6.4.2) COMPLEXED WITH FAD (*see also*, accession number P06715), which includes LPALP (SEQ ID NO:95), and PALP (SEQ ID NO:184);

Accession number pdb|1PBW|1PBW-A STRUCTURE OF BCR-HOMOLOGY (BH) DOMAIN (*see also*, accession number P27986), which includes PALP (SEQ ID NO:184);

Accession number pdb|1BBS|1BBS RENIN (E.C.3.4.23.15), which includes MPALP

(SEQ ID NO:96);

Accession number AI188872 11.3 366 327 18 382 [Homo sapiens]qd27c01.x1 Soares_placenta_8to9weeks_2NbHP8to9W, Homo sapiens cDNA clone IMAGE:1724928 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);, mRNA sequence.; minus strand; translated, which includes MXRVLQGVLPALPQVVC (SEQ ID NO:97), MXRV (SEQ ID NO:98), and MXR;

Accession number AI126906 19.8 418 343 1 418 [Homo sapiens]qb95f01.x1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:1707865 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);, mRNA sequence.; minus strand; translated, which includes ITRVMQGVIPALPQVVC (SEQ ID NO:99);

Accession number AI221581 29.1 456 341 23 510 [Homo sapiens]qg20a03.x1 Soares placenta 8 to 9 weeks 2NbHP8to9W Homo sapiens cDNA clone IMAGE:1760044 3' similar to gb:J00117 CHORIOGONADOTROPIN BETA CHAIN PRECURSOR (HUMAN);, mRNA sequence.; minus strand; translated, which includes MTRVLQVVLLALPQLV (SEQ ID NO:100);

Accession number Mm.42246.3 Mm.42246 101.3 837 304 28 768 GENE=Pck1 PROTSIM=pir:T24168 phosphoenolpyruvate carboxykinase 1, cytosolic; translated, which includes KVIQGSLSLPQAV (SEQ ID NO:101), LDSL (SEQ ID NO:102), and LPQ;

Accession number Mm.22430.1 Mm.22430 209.4 1275 157 75 1535 GENE=Ask-pending PROTSIM=pir:T02633 activator of S phase kinase; translated, which includes VLQAILPSAPQ (SEQ ID NO:103), LQA, LQAIL (SEQ ID NO:104), PSAP (SEQ ID NO:105), and LPS;

Accession number Hs.63758.4 Hs.63758 93.8 3092 1210 51 2719 GENE=TFR2 PROTSIM=pir:T30154 transferrin receptor 2; translated, which includes KVLQGRLPAVAQAV (SEQ ID NO:106), LQG, LPA, and LPAV (SEQ ID NO:107);

Accession number Mm.129320.2 Mm.129320 173.0 3220 571 55 2769 GENE= PROTSIM=pir:T16409 Sequence 8 from Patent WO9950284; translated, which includes LVQKVVPMLPRLLC (SEQ ID NO:108), LVQ, LPRL (SEQ ID NO:109), and PMLP (SEQ ID

NO:110);

Accession number Mm.22430.1 Mm.22430 209.4 1275 157 75 1535 GENE=Ask-pending PROTSIM=pir:T02633 activator of S phase kinase; translated, which includes VLQAILPSAPQ (SEQ ID NO:103), LQA, LQAIL (SEQ ID NO:104), PSAP (SEQ ID NO:105), and PSAPQ (SEQ ID NO:111);

Accession number P20155 IAC2_HUMAN Acrosin-trypsin inhibitor II precursor (HUSI-II) [SPINK2] [Homo sapiens], which includes LPGCPRHFNPV (SEQ ID NO:112), LPG, and LPGC (SEQ ID NO:41);

Accession number Rn.2337.1 Rn.2337 113.0 322 104 1 327 GENE=PROTSIM=PRF:1402234A Rat pancreatic secretory trypsin inhibitor type II (PSTI-II) mRNA, complete cds; minus strand; translated, which includes LVGCPRDYDPV (SEQ ID NO:113), LVG, and LVGC (SEQ ID NO:114);

Accession number Hs.297775.1 Hs.297775 43.8 1167 753 31 1291 GENE=PROTSIM=sp:O00268 ESTs, Weakly similar to T2D3_HUMAN TRANSCRIPTION INITIATION FACTOR TFIID 135 KDA SUBUNIT [H.sapiens]; minus strand; translated, which includes PGCPRG (SEQ ID NO:115), and PGCP (SEQ ID NO:10);

Accession number Mm.1359.1 Mm.1359 PROTSTM=pir.A39743 urokinase plasmiogen activator receptor, which includes LPGCP (SEQ ID NO:116), PGCP (SEQ ID NO:10), LPG, and LPGC (SEQ ID NO:41);

Accession number sptrembl|O56177|O56177 ENVELOPE GLYCOPROTEIN, which includes VLPAAP (SEQ ID NO:117), and PAAP (SEQ ID NO:72);

Accession number sptrembl|Q9W234|Q9W234 CG13509 PROTEIN.//:trembl|AE003458|AE003458_7 gene: "CG13509"; Drosophila melanogaster genomic scaffold, which includes LAGTIPATP (SEQ ID NO:118), LAG, and PATP (SEQ ID NO:119);

Accession number swiss|P81272|NS2B_HUMAN NITRIC-OXIDE SYNTHASE IIB (EC 1.14.13.39) (NOS, TYPE II B) (NOSIIB) (FRAGMENTS), which includes GVLPAVP, LPA, VLPAVP (SEQ ID NO:12), and PAVP (SEQ ID NO:311);

Accession number sptrembl|O30137|O30137 HYPOTHETICAL 17.2 KDA, which

includes GVLPALP (SEQ ID NO:32), PALP (SEQ ID NO:184), and LPAL (SEQ ID NO:183);

Accession number [sptrembl|Q9IYZ3|Q9IYZ3](#) DNA POLYMERASE, which includes GLLPCLP (SEQ ID NO:120), LPC, LPCL (SEQ ID NO:88), and PCLP (SEQ ID NO:89);

Accession number [sptrembl|Q9PVW5|Q9PVW5](#) NUCLEAR PROTEIN NP220, which includes PGAP (SEQ ID NO:121), LPQRPRGPNP (SEQ ID NO:122), LPQ, PRGP (SEQ ID NO:123), and PNP;

Accession number [Hs.303116.2](#) PROTSIM=[pir](#);T33097 stromal cell-derived factor 2-like1; translated, which includes GCPR (SEQ ID NO:124);

Accession number [pdb|1DU3|1DU3-A](#) CRYSTAL STRUCTURE OF TRAIL-SDR5, which includes GCPRGM (SEQ ID NO:125);

Accession number [pdb|1D0G|1D0G-R](#) CRYSTAL STRUCTURE OF DEATH RECEPTOR 5 (DR5) BOUND TO APO2L/TRAIL, which includes GCPRGM (SEQ ID NO:125);

Accession number [pdb|1BIO|1BIO](#) HUMAN COMPLEMENT FACTOR D IN COMPLEX WITH ISATOIC ANHYDRIDE INHIBITOR, which includes LQHV (SEQ ID NO:126);

Accession number [pdb|4NOS|4NOS-A](#) HUMAN INDUCIBLE NITRIC OXIDE SYNTHASE WITH INHIBITOR, which includes FPGC (SEQ ID NO:9), and PGCP (SEQ ID NO:10);

Accession number [pdb|1FL7|1FL7-B](#) HUMAN FOLLICLE STIMULATING HORMONE, which includes PARP (SEQ ID NO:62), and VPGC (SEQ ID NO:127);

Accession number [pdb|1HR6|1HR6-A](#) YEAST MITOCHONDRIAL PROCESSING PEPTIDASE, which includes CPRG (SEQ ID NO:128), and LKGC (SEQ ID NO:129);

Accession number [pdb|1BFA|1BFA](#) RECOMBINANT BIFUNCTIONAL HAGEMAN FACTOR/AMYLASE INHIBITOR FROM, which includes PPGP (SEQ ID NO:130), LPGCPREV (SEQ ID NO:131), LPGC (SEQ ID NO:41), PGCP (SEQ ID NO:10), and CPRE (SEQ ID NO:132);

Accession number [swissnew|P01229|LSHB_HUMAN](#) Lutropin beta chain precursor, which includes MMRVLQAVLPPLPQVVC (SEQ ID NO:133), MMR, MMRV (SEQ ID

NO:383 134), LQA, LQAV (SEQ ID NO:52), VLPPLP (SEQ ID NO:135), PPLP (SEQ ID NO:82), QVVC (SEQ ID NO:43), VVC, VLPPLPQ (SEQ ID NO:136), AVLPPPLP (SEQ ID NO:137), and AVLPPPLPQ (SEQ ID NO:138);

Accession number swissnew|P07434|CGHB_PAPAN Choriogonadotropin beta chain precursor, which includes MMRVLQAVLPPVPQVVC (SEQ ID NO:312), MMR, MMRV (SEQ ID NO:134), LQA, LQAG (SEQ ID NO:140), VLPPVP (SEQ ID NO:141), VLPPVPQ (SEQ ID NO:142), QVVC (SEQ ID NO:43), VVC, AVLPPVP (SEQ ID NO:143), and AVLPPVPQ (SEQ ID NO:144);

Accession number swissnew|Q28376|TSHB_HORSE Thyrotropin beta chain precursor, which includes MTRD (SEQ ID NO:145), LPK, QDVC (SEQ ID NO:146), DVC, IPGC (SEQ ID NO:147), and PGCP (SEQ ID NO:10);

Accession number swissnew|P95180|NUOB_MYCTU NADH dehydrogenase I chain B, which includes LPGC (SEQ ID NO:41), and PGCP (SEQ ID NO:10);

Accession number sptrembl|Q9Z284|Q9Z284 NEUTROPHIL ELASTASE, which includes PALP (SEQ ID NO:184), and PALPS (SEQ ID NO:148);

Accession number sptrembl|Q9UCG8|Q9UCG8 URINARY GONADOTROPHIN PEPTIDE (FRAGMENT), which includes LPGGPR (SEQ ID NO:149), LPG, LPGG (SEQ ID NO:150), and GGPR (SEQ ID NO:151); and

Accession number XP_028754 growth hormone releasing hormone [Homo sapiens], which includes LQRG (SEQ ID NO:152), LQRGV (SEQ ID NO:153), and LGQL (SEQ ID NO:154). All of which are hereby incorporated in their entirety by reference.

Furthermore, please amend Table 1 on page 29 as follows:

TABLE 1. Results of shock experiments in mice

TEST SUBSTANCE (HRS)	% SURVIVAL IN TIME			
	0	16	40	72
PBS	100	100	67	17
PG23	100	100	100	100

PG25		100	83	83	83
PEPTIDE					
NMPF	SEQUENCE				
1	VLPALPQVVC (SEQ ID NO:20)	100	100	50	17
2	LQGVLPALPQ (SEQ ID NO:49)	100	67	0	0
3	LQG	100	83	20	17
4	LQGV (SEQ ID NO:1)	100	100	100	100
5	GVLPALPQ (SEQ ID NO:33)	100	100	80	17
6	VLPALP (SEQ ID NO:3)	100	100	100	100
7	VLPALPQ (SEQ ID NO:468 <u>29</u>)	100	83	0	0
8	GVLPALP (SEQ ID NO:32)	100	100	83	67
9	VVC	100	100	50	50
11	MTRV (SEQ ID NO:42)	100	100	67	50
12	MTR	100	100	67	50
13	LQGVLPALPQVVC (SEQ ID NO:34)	100	100	100	100
14	(CYCLIC) LQGVLPALPQVVC (SEQ ID NO:34)	100	83	83	83
64	LPGCPRGVNPVVS (SEQ ID NO:40)	100	100	100	100
66	LPGC (SEQ ID NO:41)	100	100	100	100